

# SEQUENCE LISTING

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<120> THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc  
EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN IgE  
ANTIBODY AND USES THEREOF

<130> AL-8

<140> not yet assigned

<141> 2001-03-14

<150> 60/189,853

<151> 2000-03-15

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 528

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(528)

<400> 1

gtc cct cag aaa cct aag gtc tcc ttg aac cct cca tgg aat aga ata	48
Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile	
1 5 10 15	

ttt aaa gga gag aat gtg act ctt aca tgt aat ggg aac aat ttc ttt	96
Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe	
20 25 30	

gaa gtc agt tcc acc aaa tgg ttc cac aat ggc agc ctt tca gaa gag	144
Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu	
35 40 45	

aca aat tca agt ttg aat att gtg aat gcc aaa ttt gaa gac agt gga	192
Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly	
50 55 60	

gaa tac aaa tgt cag cac caa caa gtt aat gag agt gaa cct gtg tac 240  
 Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr  
 65 70 75 80

ctg gaa gtc ttc agt gac tgg ctg ctc ctt cag gcc tct gct gag gtg 288  
 Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val  
 85 90 95

gtg atg gag ggc cag ccc ctc ttc ctc agg tgc cat ggt tgg agg aac 336  
 Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn  
 100 105 110

tgg gat gtg tac aag gtg atc tat tat aag gat ggt gaa gct ctc aag 384  
 Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys  
 115 120 125

tac tgg tat gag aac cac aac atc tcc att aca aat gcc aca gtt gaa 432  
 Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu  
 130 135 140

gac agt gga acc tac tac tgt acg ggc aaa gtg tgg cag ctg gac tat 480  
 Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr  
 145 150 155 160

gag tct gag ccc ctc aac att act gta ata aaa gct ccg cgt gag aag 528  
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 165 170 175

<210> 2

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<212> PRT

<213> Homo sapiens

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Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile  
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Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe  
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Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu  
 35 40 45

Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly  
 50 55 60

Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr  
65 70 75 80

Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val  
85 90 95

Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn  
100 105 110

Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys  
115 120 125

Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu  
130 135 140

Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr  
145 150 155 160

Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys  
165 170 175

<210> 3

<211> 528

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(528)

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Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile  
1 5 10 15

ttt aaa gga gag aat gtg act ctt aca tgt aat ggg aac aat ttc ttt 96  
Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe  
20 25 30

gaa gtc agt tcc acc aaa tgg ttc cac aat ggc agc ctt tca gaa gag 144  
Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu  
35 40 45

aca aat tca agt ttg aat att gtg aat gcc aaa ttt gaa gac agt gga 192  
Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly  
50 55 60

gaa tac aaa tgt cag cac caa caa gtt gct gag agt gaa cct gtg tac 240  
 Glu Tyr Lys Cys Gln His Gln Gln Val Ala Glu Ser Glu Pro Val Tyr  
 65 70 75 80

ctg gaa gtc ttc agt gac tgg ctg ctc ctt cag gcc tct gct gag gtg 288  
 Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val  
 85 90 95

gtg atg gag ggc cag ccc ctc ttc ctc agg tgc cat ggt tgg agg aac 336  
 Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn  
 100 105 110

tgg gat gtg tac aag gtg atc tat tat aag gat ggt gaa gct ctc aag 384  
 Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys  
 115 120 125

tat tgg tat gag aac cac gct atc tcc att aca aat gcc gca gct gaa 432  
 Tyr Trp Tyr Glu Asn His Ala Ile Ser Ile Thr Asn Ala Ala Glu  
 130 135 140

gac agt gga acc tac tac tgt acg ggc aaa gtg tgg cag ctg gac tat 480  
 Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr  
 145 150 155 160

gag tct gag ccc ctc aac att act gta ata aaa gct ccg cgt gag aag 528  
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 165 170 175

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<212> PRT

<213> Homo sapiens

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Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile  
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Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe  
 20 25 30

Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu  
 35 40 45

Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly  
 50 55 60

Glu Tyr Lys Cys Gln His Gln Gln Val Ala Glu Ser Glu Pro Val Tyr  
65 70 75 80

Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val  
85 90 95

Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn  
100 105 110

Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys  
115 120 125

Tyr Trp Tyr Glu Asn His Ala Ile Ser Ile Thr Asn Ala Ala Ala Glu  
130 135 140

Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr  
145 150 155 160

Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys  
165 170 175

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<213> Homo sapiens

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<221> CDS

<222> (1)..(666)

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1 5 10 15

cgg ccc agc ccg ttc gac ctg ttc atc cgc aag tcg ccc acg atc acc 96  
Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr  
20 25 30

tgt ctg gtg gtg gac ctg gca ccc agc aag ggg acc gtg aac ctg acc 144  
Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr  
35 40 45

tgg tcc cgg gcc agt ggg aag cct gtg aac cac tcc acc aga aag gag 192  
Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu  
50 55 60

gag aag cag cgc aat ggc acg tta acc gtc acg tcc acc ctg ccg gtg 240  
 Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val  
 65 70 75 80

ggc acc cga gac tgg atc gag ggg gag acc tac cag tgc agg gtg acc 288  
 Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr  
 85 90 95

cac ccc cac ctg ccc agg gcc ctc atg cgg tcc acg acc aag acc agc 336  
 His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser  
 100 105 110

ggc ccg cgt gct gcc ccg gaa gtc tat gcg ttt gcg acg ccg gag tgg 384  
 Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp  
 115 120 125

ccg ggg agc cgg gac aag cgc acc ctc gcc tgc ctg atc cag aac ttc 432  
 Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe  
 130 135 140

atg cct gag gac atc tcg gtg cag tgg ctg cac aac gag gtg cag ctc 480  
 Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu  
 145 150 155 160

ccg gac gcc cgg cac agc acg acg cag ccc cgc aag acc aag ggc tcc 528  
 Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser  
 165 170 175

ggc ttc ttc gtc ttc agc cgc ctg gag gtg acc agg gcc gaa tgg gag 576  
 Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu  
 180 185 190

cag aaa gat gag ttc atc tgc cgt gca gtc cat gag gca gcg agc ccc 624  
 Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro  
 195 200 205

tca cag acc gtc cag cga gcg gtg tct gta aat ccc ggt aaa tga 669  
 Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys  
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Ala Asp Pro Cys Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser  
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Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr  
 20 25 30

Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr  
 35 40 45

Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu  
 50 55 60

Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val  
 65 70 75 80

Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr  
 85 90 95

His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser  
 100 105 110

Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp  
 115 120 125

Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe  
 130 135 140

Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu  
 145 150 155 160

Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser  
 165 170 175

Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu  
 180 185 190

Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro  
 195 200 205

Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys  
 210 215 220